CLAIMS

WHAT IS CLAIMED IS:

1. A catalytic hybridization composition comprising:

a probe containing at least one probe nucleobase sequence and at least one scissile linkage sequence;

an enzyme adapted to cleave said at least one scissile linkage sequence;

a nucleic acid target containing at least one target nucleobase sequence associated with said nucleobase sequence of said probe by Watson-Crick bonding to form a multiplex structure; and

a hybridization medium containing said probe, said enzyme and said nucleic acid target,

wherein at least one of said probe nucleobase sequence and said target nucleobase sequence is double-stranded.

2. The composition of claim 1, wherein at least a portion of said multiplex structure is isolated, purified, artificial or synthetic triplex.

3. The composition of claim 1, wherein said probe is single stranded and said target is double stranded.

4. The composition of claim 1, wherein at least a portion of said probe is double stranded.

5. The composition of claim 4, wherein at least a portion of one strand of said probe comprises RNA, mRNA, hnRNA, tRNA or cDNA.

6. The composition of claim 1, wherein at least a portion of said multiplex structure is an isolated, purified, artificial or synthetic quadruplex.

7. The composition of claim 6, wherein a major groove of said probe is placed in a major groove of said target.

8. The composition of claim 6, wherein a major groove of said probe is placed in a minor groove of said target.

9. The composition of claim 1, wherein at least a portion of said probe comprises a nucleic acid or a nucleic acid analogue.

10. The composition of claim 1, wherein at least a portion of said probe comprises a nucleic acid analogue containing an uncharged or partially charged backbone.

11. The composition of claim 1, wherein each nucleobase binds to no more than two other nucleobases.

12. The composition of claim 1, wherein said composition is substantially free of self-hybridized strands.

13. The composition of claim 1, wherein said multiplex structure is substantially free of Hoogsteen binding.

14. The composition of claim 1, wherein said multiplex structure is substantially free of G-G quartets.

15. The composition of claim 1, wherein said probe is 5 to 75 nucleobases.

16. The composition of claim 1, wherein said target is genomic DNA.

17. The composition of claim 1, wherein said target includes a haplotype in genomic DNA.

18. The composition of claim 1, wherein said target comprises PCR amplified products.

19. The composition of claim 1, wherein said multiplex structure is free of solid support.

20. The composition of claim 1, wherein said multiplex structure is bound to a solid support.

21. The composition of claim 20, wherein said solid support is not electrically conductive.

22. The composition of claim 20, wherein said solid support is electrically conductive.

23. The composition of claim 1, wherein said at least one probe nucleobase sequence is from 2 to 30 bases long and said target is at least 8 base pairs long.

24. A method for assaying binding, said method comprising:

providing a probe containing at least one probe nucleobase sequence and at least one scissile linkage sequence;

providing an enzyme adapted to cleave said at least one scissile linkage sequence;

providing a target containing at least one target nucleobase sequence;

combining said probe, said enzyme and said target in a hybridization medium further containing water, a buffer and at least one promoter;

incubating said hybridization medium to hybridize said probe nucleobase sequence to said target nucleobase sequence by Watson-Crick bonding to form a multiplex, wherein at least one of said probe nucleobase sequence

and said target nucleobase sequence is double-stranded;

cleaving hybridized probes at said at least one scissile linkage to provide unbound probe fragments; and

detecting said unbound probe fragments to assay binding between said probe and said target.

25. The method of claim 24, wherein an incubation temperature is from 2°C to 60°C.

26. The method of claim 24, wherein said hybridization medium is buffered to a pH of about 5 to about 9.

27. The method of claim 24, wherein said at least one promoter is an intercalating agent.

28. The method of claim 27, wherein said at least one promoter is an intercalating fluorophore, and a fluorescent intensity of a test medium containing said multiplex structure is directly correlated with a binding affinity of said probe for said target.

29. The method of claim 28, wherein said intercalating fluorophore is a member selected from the group consisting of YOYO-1, TOTO-1, ethidium bromide, ethidium homodimer-1, ethidium homodimer-2 and acridine.

30. The method of claim 24, wherein said at least one promoter is tethered to said probe.

31. The method of claim 24, wherein said at least one promoter is a monovalent cation.

32. The method of claim 24, wherein said at least one promoter is a cation having a valency greater than one.

33. The method of claim 32, wherein said at least one promoter is at least one member selected from the group consisting of alkali metal cations, alkaline earth metal cations, transition metal cations, $Co(NH_3)_6^{+3}$, trivalent spermidine and tetravalent spermidine.

34. The method of claim 32, wherein said cation is K^+ or Na^+ provided at a concentration of 40 mM to 200 mM.

35. The method of claim 24, wherein said target is provided in said hybridization medium before said probe, and wherein said probe is provided in dehydrated form prior to rehydration by contact with said hybridization medium.

36. The method of claim 24, wherein said incubation time is not more than about 24 hours.

37. The method of claim 24, wherein probe-target hybridization is detected as a change in a fluorescent, chemiluminescent, electrochemiluminescent or electrical signal.

38. The method of claim 37, wherein an intensity of said signal is correlated with a binding affinity between said probe and said target.

39. The method of claim 38, wherein said probe is covalently labeled with a non-intercalating fluorophore and said intensity is inversely correlated with said binding affinity.

40. The method of claim 39, wherein said non-intercalating fluorophore is a member selected from the group consisting of biotin, rhodamine and fluorescein.

41. The method of claim 37, wherein said method is a homogeneous assay.

42. The method of claim 24, wherein said probe is covalently labeled with a marking agent on a first side of said at least one scissile linkage and a quenching agent on a second side of said at least one scissile linkage, wherein said quenching agent quenches a signal of said marking agent when said probe is intact and does not quench said signal after said probe is cleaved.

43. The method of claim 24, wherein said probe is covalently labeled with a marking agent on a first side of said at least one scissile linkage and a amplification agent on a second side of said at least one scissile linkage, wherein said amplification agent amplifies a signal of said marking agent when said probe is intact and does not amplify said signal after said probe is cleaved.

44. The method of claim 24, further comprising separating intact probes from said probe fragments.

45. The method of claim 24, wherein a ratio of said probe to said target is from 100:1 to 1000:1.

46. The method of claim 24, wherein concentrations of said probe and said target are not more than 5×10^{-10} M.

47. The method of claim 24, wherein said at least one promoter is a minor groove nucleic acid binding molecule, which binds in a non-intercalating manner and binds with an association constant of at least 10^3 M^{-1}.

48. The method of claim 24, wherein conditions of hybridization are subject to transitory or periodic changes.

49. The method of claim 48, wherein the changes are caused by applying a force.

50. The method of claim 49, wherein the force applied is electric, magnetic or mechanical.

51. The method of claim 24, wherein cleaved probe and unhybridized probe remain in solution.

52. The method of claim 24, wherein said enzyme will cleave only RNA sequences of nucleotides in a multiplex structure.

53. The method of claim 24, wherein said enzyme will cleave only nucleobases having predetermined backbone characteristics.

54. The method of claim 24, wherein a backbone structure of said probe is composed entirely of RNA.

55. The method of claim 54, wherein said at least one scissile linkage sequence is about 2 to about 12 nucleotides in length.

56. The method of claim 24, wherein said probe contains at least one interspersed sequence that is not cleavable by said enzyme.

57. The method of claim 56, wherein said at least one interspersed sequence comprises DNA or DNA analogues.

58. The method of claim 57, wherein said at least one interspersed sequence comprises nucleotide residues selected from the group consisting of phosphonates, phosphotriesters, phosphoroamidates and 2'-0 alkyl and aryl ribonucleotide.

59. The method of claim 24, further comprising suppressing non-specific cleavage of the probe with at least one single-stranded ribonuclease inhibitor selected from the group consisting of vanadate, RNAsin, and Inhibit - ACE.

60. The method of claim 24, wherein said enzyme is RNAaseH.

61. The method of claim 60, wherein said RNAaseH enzyme is obtained from E. coli.

62. The composition of claim 1, wherein said probe comprises an electrically, electromechanically or optically active reporter group adapted to emit a detectable signal.

63. An electrical circuit comprising the composition of claim 1.